# The Study of Correlation and Genetic Divergence analysis between Yield and Yield related traits of Bread Wheat (*Triticum Aestivum L.*) Genotypes

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**Abstract:** Wheat is one of the best useful crops grown in Ethiopia. Evaluation of correlation and Genetic Divergence analysis provides the basis for increasing yield and successful breeding programme. In addition, some information is generated about correlation and genetic divergence analysis between yield and yield related traits of bread wheat germplasm in Ethiopia. Therefore this study was conducted to evaluate the extent of genetic correlation and Genetic Divergence analysis among yield and yield related traits of bread wheat genotypes. The study was carried out with the following objectives; to assess the association and Genetic Divergence analysis for yield and yield related traits like genotypic and phenotypic association and Genetic Divergence analysis of yield and yield related traits. To achieve the above objectives; total of 100 bread wheat (*Triticum aestivum* L.) genotypes were evaluated at Holeta Agricultural Research Centre in 2021 main cropping season. The experiment was conducted by using 10x10 alpha lattice designs. Data were subjected to analysis of variance which revealed that there was highly significant difference (p=0.01) among the genotypes for all characters studied. The highest grain yield (5620.76t ha) was recorded from Elit Ethiopia172/2020 and the lowest grain yield (1027.2t/ha) was recorded from 30HRWSN246/2019 genotype. Grain yield was positive and highly correlated with harvest index (r=0.810), thousand kernel weight (r=0.786), kernels per spike (r=0.716), hectoliter weight (r=0.631), Plant height(r=0.347), spikelets per spike (r=0.325), and spike length (r=0.214), and negative and significant correlation with fertile tillers per plant (r=-0.1600.25). The highest cluster was clusterI which consistes of 45 genotypes (31.30%), and the lowest cluster was cluster VI (6.30%) consists of 1 genotype.

**Keywords:** Correlation, Genetic Divergence, Variability, Cluster.

# INTRODUCTION

Bread wheat (*Triticum aestivum* L.), is a hexaploid species with 2n=6x=42, and a self-pollinating annual plant in the true grass family Gramineae (Poaceae). It is the largest cereal crop extensively grown as staple food sources in the world (Mollasadeghi *et al.*, 2011). It is one of the most important export and strategic cereal crop in the world and in Ethiopia in terms of production and utilization (Ranjana *et al.*, 2013). Bread wheat has been described as the 'King of cereals' because of the prominent position it holds and largest it occupies, high productivity in the international food grain trade (Rathwa *et al.*, 2018). Currently it is also becoming most important cereals grown on a large scale (Alemayehu Seyoum *et al.*, 2011). Because of its significance as cash crop, high level of production per unit area, and its major role in supplying the dietary requirements of the society. Wheat is grown at an altitude ranging from 1500 to 3000 m.a.s.l, between 6-16° N latitude and 35-42° E longitude in our country. Bread wheat falls between 1900 and 2700 m.a.s.l (Abu Tefera, 2012). Next to sub-Sahara Africa, Ethiopia is the largest wheat producer in terms of total wheat area coverage and production. It ranks fourth after teff (*Eragrostis tef*), maize (*Zea mays*) and sorghum (*Sorghum bicolar*) in total area coverage of 1.7 million ha and third in total production of 4.6 million tons next to teff and maize with productivity of 2.74t/ha from cereals in different regions of Ethiopia (CSA, 2018). The main wheat producing areas in Ethiopia are located in Oromiya (Arsi, Bale, Shewa, Ilubabor, and Western Hararghe), in SNNPR (Hadiya, Sidamo, Silte, Guraghe, Kambata), Tigray, Amhara (Northern Gondar and Gojam zones). The productivity of wheat in Amhara region is 2.53 t/ha (CSA, 2018).

Genetic correlation among and with breeding materials can be identified and classified using multivariate grouping methods, for classifying breeding

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materials into distinct and variable groups depending on genotype performance (Aremu CO, 2012). Multivariate statistical analysis is done by one of the most efficient and common method of Cluster analysis for grouping genotypes. From the most common method of Cluster analysis, Wards method is the one (Karamanos AJ *et al.*, 1998). Clustering of individuals should then exhibit internal (within the cluster) homogeneity and high external (between clusters) heterogeneity, thus, if the classification is successful, it is better, when individuals within a cluster is closer when plotted geometrically and different clusters shall be farther apart.

Genetic distance is defined as the difference between two entities that can be described by allelic variation (Nei M., 1973). Mahalanobis generalized distances approach, adopting, multiple measurements provided a measure of the generalized distance (Mahalanobis PC, 1936). This method of measurement was important for the identification of genetically divergent genotypes to facilitate the grouping and characterization of agronomic and morphological characteristics (Morishima H *et al.*, 1960). In addition, this study also permitted the choice of genetically different parents to obtain desirable recombinants in segregating generations. Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar to each other than to those in other groups (clusters). Based on quantitative data, bread wheat genotypes were grouped by cluster analysis on the basis of Euclidean distances of similarity to their distinct groups. Therefore the objective of the study was to Evaluation of Correlation and Genetic Divergence analysis between Yield and Yield related traits of Bread Wheat.

# MATERIAL AND METHOD
The experiment was conducted at the main station of Holeta Agricultural Research Centre (HARC). A total of 100 genotypes including two released varieties, namely (Alidoro) and Dendaa were evaluated in this study. The genotypes were planted in July 2021 at Holeta Agricultural Research Center in alpha lattice design with two replications, each consisting of 10 incomplete blocks with 100 genotypes in each replication. Each plots consisted of six rows each 2.5 m long by 1.2 m wide (3 m$^2$), with 0.2 m spacing between rows. The spacing between plots, blocks in each replication, and between replications were 0.5, 1, and 1.5 m, respectively.

## Data Collected
Data was collected from the mean of then plants randomly selected from each plot. Those were number of days to heading, grain filling period, plant height, spike length, above ground biomass, grain yield, days to maturity, harvest index, hectoliter weight, thousand kernel weight, spikelet per spike, kernel per spike, fertile tiller per plant were collected.

## Data Analysis
## Estimation of Correlation between Traits
Phenotypic and genotypic correlation coefficients based on the mean data of the bread wheat genotypes from corresponding variance and covariance components were estimated according to the procedures suggested by (Dabholkar, 1992):

➢ Phenotypic coefficient of correlation (rp)
rp= Pcovxy/ $\sqrt{(\sigma^2px . \sigma^2py)}$

➢ Genotypic coefficient of correlation (rg)
rg= Gcovxy/ $\sqrt{(\sigma^2gx . \sigma^2gy)}$

Where: rp = Phenotypic correlation coefficient
rg = Genotypic correlation coefficient
Pcovxy = Phenotypic covariance between variables x and y
Gcovxy = Genotypic covariance between variables x and y
$\sigma^2g$ x=Genotypic variance for trait X
$\sigma^2g$ y=Genotypic variance for trait Y
$\sigma^2px$=Phenotypic variance for trait X
$\sigma^2py$=Phenotypic variance for trait Y

The significance of phenotypic correlation coefficients was tested by the formula of Singh and Chaudhary (1985).

$$t' = r_{pxy} * \sqrt{\frac{g-2}{(1-rp^2xy)}}$$

t' value was tested against the tabulated t-value for (g-2) degree of freedom where g was the number of genotypes studied.

Whereas the significance of the genotypic correlation coefficient was tested using the formula described by Robertson (1959) indicated as

$t' = \frac{rg_{xy}}{SE_{gxy}}$ and SE= $\sqrt{\frac{1-rg^2xy}{2hx*hy}}$ where h$_x$= heritability of traits x, h$_y$=heritability of traits y, g=number of genotypes, and rgxy = genotypic correlation coefficient. Thus, the calculated value was compared with the tabulated value at g-2 degrees of freedom at 5% and 1% level of significance.

## Cluster Analysis
In this study unweighted Pair Group Method with Arithmetic Mean (UPGMA) clustering method was used for cluster analysis from Euclidean distance matrix. Genetic divergence analysis has been used to classify the divergent genotypes into different groups using Euclidean distance (ED) calculated from quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Mohammadi and Prasanna (2003) as follows;

Where; EDjk = distance between genotypes j and k; Xij and Xik = phenotype traits values of the ith

character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance.

**Correlation of the Studied Traits**

The results indicated that at the phenotypic level there was a positive and highly significant correlation of grain yield with harvest index (r=0.810), thousand kernel weight (r=0.786), kernels per spike (r=0.716), hectoliter weight (r=0.631), Plant height (r=0.347), spikelets per spike (r=0.325), and spike length (r=0.214), and negative and significant correlation with fertile tillers per plant (r=-0.1600.25) (Table 8). Wasif *et al.*, (2015) reported significant positive phenotypic correlations of above-ground biomass, kernels per spike and plant height with grain yield. The same auther reported a non-significant correlation of thousand kernel weight and harvest index with grain yield which contradicted our finding. Quan (2015) also reported positive correlations of grain yield with above-ground biomass, harvest index, kernels per spike, which are in agreement with our study findings. Recent yield improvement has shown an association with increased biomass (Sadras and Lawson, 2011). Foulkes *et al.*, (2011) reported high biomass is an especially valuable trait to raise the yield potential of bread wheat, because HI is approaching the limit of approximately 0.64, and there has been no significant progress since the early 1990s (0.50-0.55). Among the studied characters, harvest index is the most important physiological trait. A similar association in winter wheat was also reported by Majumder *et al.*, (2008). Grain yield showed non-significant negative phenotypic correlation with the rest of the traits.

Days to heading showed positive significant correlation with days to maturity (0.350), above-ground biomass (0.214), grain yield (0.165), hectoliter weight (0.152), plant height (0.158), spikelets per spike (0.402), spike length (0.157), kernels per spike (0.236), and negative correlation with grain filling period (r= -0.483), and total number of tillers per plant (r=-0.180). The result is in agreement with Awale *et al.*, (2013) for the association of days to heading with days to maturity and grains filling period. Grain filling period showed positive significant correlation with days to maturity (0.559), above-ground biomass (0.197), grain yield (0.174), and thousand kernel weight (0.251). Days to maturity showed positive significant correlation with above-ground biomass (0.367), grain yield (0.290), thousand kernel weight (0.268), plant height (0.162), and spikelets per spike (0.308), kernels per spike (0.260). Above-ground biomass showed a positive significant correlation with grain yield (0.620), harvest index (0.238), hectoliter weight (0.391), and thousand kernel weight (0.533), and plant height (0.351), spikelets per spike (0.413), spike length (0.168), and kernels per spike (0.519).

Harvest index showed a positive significant correlation with hectoliter weight (0.688), thousand kernel weight (0.715), plant height (0.212), kernels per spike (0.617), and negative correlation with fertile tillers per plant (-0.170). Hectoliter weight showed a positive significant correlation with thousand kernel weight (0.678), plant height (0.154), spikelets per spike (0.142), kernels per spike (0.573), and negative correlation with the total number of tillers per plant (-0.141).

Thousand kernel weight showed a positive significant correlation with plant height (0.344), spikelets per spike (0.163), kernel per spike (0.551), and negative significant correlation with fertile tillers per plant (-0.243). Quan (2015) reported that 1000 kernel weight was consistently negatively associated with grains per spike, but in this study they have a positive association between them.

Plant height showed a positive significant correlation with spikelets per spike (0.225), and kernels per spike (0.250). Spikelets per spike showed a positive significant correlation with spike length (0.437), and kernels per spike (0.491). Spike length showed a positive significant correlation with kernels per spike (0.244). Spike length and kernels per spike showed a highly positive correlation with each other which is in agreement with the finding of Wasif *et al.*, (2015). Similarly, Obsa (2014) reported positive and significant correlation of spike length with plant height and kernels per spike, suggesting the genotypes with longer spike length may also be longer in plant height with more number of kernels per spike. It also showed significant positive correlation at genotypic level with plant height and spikelets per spike. Fertile tillers per plant showed positive significant correlation with total number of tillers per plant (0.572).

At the genotypic level, grain yield showed a highly positive significant correlation with harvest index (0.827), hectoliter weight (0.634), thousand kernel weight (0.793), plant height (0.352), spikelets per spike (0.350), spike length (0.347), kernels per spike (0.719), and a highly negative significant correlation with fertile tillers per plant (-0.193) and total number of tillers per plant (-0.087). Balcha, (2002) observed that grain yield was positively correlated with grain filling period, spike length, and harvest index, but negatively correlated with days to heading and maturity, plant height, and thousand kernel weights. Similarly, grain yield was correlated with those traits, but the correlation was positive. Days to heading showed highly positive significant correlation with days to maturity (0.361), above-ground biomass (0.226), grain yield (0.167), harvest index (0.102), hectoliter weight (0.158), thousand kernel weight (0.072), plant height (0.162), spikelets per spike (0.438), spike length (0.227), kernels per spike (0.238), and a highly negative correlation with grain filling period (-0.494), and negative significant correlation with the total number of tillers per plant (-0.189). Grain filling period showed a highly positive significant correlation with days to maturity (0.573), above-ground biomass (0.204), grain yield (0.179), thousand kernel weight (0.256), plant

height (0.048), the total number of tillers per plant (0.046), kernels per spike (0.062), and a highly negative correlation with hectoliter weight (-0.007), and spikelet per spike (-0.048).

Days to maturity had a highly positive correlation with above ground biomass (0.384), grain yield (0.295), harvest index (0.059), hectoliter weight (0.103), thousand kernel weight (0.273), plant height (0.167), spikelets per spike (0.317), kernels per spike (0.265), and a highly negative correlation with total number of tillers per plant (-0.072).

Above-ground biomass showed a highly positive significant association with grain yield (0.648), harvest index (0.249), hectoliter weight (0.407), thousand kernel weight (0.556), plant height (0.378), and spikelets per spike (0.453), kernels per spike (0.536). This indicated that the increase of these characters results in increase of above ground biomass. In line with this study, biomass yield (r=0.8) had a positive and significant correlation with grain yield (Birhanu, 2010).

Harvest index showed a highly positive correlation with hectoliter weight (0.705), thousand kernel weight (0.733), plant height (0.213), spikelets per spike (0.145), spike length (0.226), kernels per spike (0.630), and a highly negative correlation with fertile tillers per plant (-0.221), and a total number of tillers per plant (-0.105). This showed that when yield components increased harvest index also increased, however fertile tillers per plant which increases yield decreased the harvest index, this could be due to its increasing effect on the biomass. In contrasts with this study, a reduction in height results in an increase in yield of wheat, which appears to be contributing to an increase in harvest HI (Richards *et al.,* 2001) which indicated that plant height and harvest index had indirect relationship, but this study showed direct relationship between plant height harvest index.

Thousand kernel weight showed a highly positive correlation with plant height (0.349), spikelets per spike (0.181), kernels per spike (0.556), and a highly negative correlation with fertile tillers per plant (-0.301), and a total number of tillers per plant (-0.102). Hectoliter

weight showed a highly positive correlation with thousand kernel weight (0.684), plant height (0.155), spikelets per spike (0.149), spike length (0.114), kernels per spike (0.577), and a highly negative correlation with fertile tillers per plant (-0.145), and a total number of tillers per plant (-0.140). The negative correlation of hectoliter weight with tillers per plant could be the consequence of competition between the vegetative parts and grains for assimilates which resulted in low accumulation of assimilates in grains.

Plant height showed a highly positive correlation with spikelets per spike (0.251), spike length (0.179), kernels per spike (0.257), and a highly negative correlation with fertile tillers per plant (-0.109). This showed that taller genotypes had longer spike with more spikeletes and grains per spike, and the negative association of plant height with tillers per plant could the competition of plants for moisture and nutrients. Genotypes with less number of tillers per plant may be faced less competition among tillers than those with more tillers per plant. Similarly, Awale *et al.,* (2013) reported that Plant height displayed a positive and highly significant association with the number of spikelets per spike at the genotypic level. In addition, plant height had a positive and significant correlation with biomass yield (r=0.34). That is genotypes with taller height had high biomass. Khan *et al.,* (2013) reported a significant and positive correlation of plant height with 1000-grain weight at both genotypic and phenotypic levels, which is in line of the finding of this study.

Spikelets per spike showed a highly significant positive correlation with spike length (0.654), and kernels per spike (0.527). Spike length had a highly significant positive correlation with kernels per spike (0.378). Fertile tillers per plant showed a highly positive correlation with a total number of tillers per plant (0.659). Total number of tillers per plant indicated a highly negative correlation with kernel per spike (-0.077). Camargo and Deo (1998) observed that grain number per ear was negatively correlated with 1000-grain weight (r = -0.91). This is because of low amount assimilate accumulation in grain due to low sharing of assimilates among more number of grains per spike.

**Table 1: Estimates of phenotypic (below diagonal) and genotypic (above diagonal) correlation coefficients among various traits of wheat genotypes grown at HARC, main station**

|  | NDH | GFP | DM | ABM | GYPHa | HI | HLW | TKW | PH | SPS | SL | FTPP | TNTPP | Kps |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NDH |  | -0.494** | 0.361** | 0.226** | 0.167*** | 0.102** | 0.158** | 0.072** | 0.162** | 0.438** | 0.227** | -0.104ns | -0.189* | 0.238** |

| | GFP | DM | AGB | GYPHa | HI | HLW | TKW | PH | SPS | SL | FTPP | TNTPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **NDH** | -0.483** | 0.350** | 0.214** | 0.165* | 0.096ns | 0.152* | 0.071ns | 0.158* | 0.402** | 0.157* | -0.081ns | -0.180* |
| **GFP** | | 0.559** | 0.197** | 0.174* | -0.022ns | -0.007ns | 0.251** | 0.045ns | -0.043ns | -0.095ns | -0.046ns | 0.048ns |
| **DM** | 0.573** | | 0.367** | 0.290** | 0.055ns | 0.100ns | 0.268** | 0.162* | 0.308** | 0.012ns | -0.075ns | -0.069ns |
| **ABM** | 0.204** | 0.384** | | 0.648** | 0.238** | 0.391** | 0.533** | 0.351** | 0.413** | 0.168* | -0.100ns | -0.008ns |
| **GYPHa** | 0.179** | 0.295** | 0.648** | | 0.810** | 0.631** | 0.786** | 0.347** | 0.325** | 0.214** | -0.160* | -0.085ns |
| **HI** | 0.020ns | 0.059** | 0.249** | 0.827** | | 0.688** | 0.715** | 0.212** | 0.124ns | 0.134ns | -0.170* | 0.105ns |
| **HLW** | -0.007** | 0.103** | 0.407** | 0.634** | 0.705** | | 0.678** | 0.154* | 0.142* | 0.074ns | -0.125ns | -0.141* |
| **TKW** | 0.256** | 0.273** | 0.556** | 0.793** | 0.733** | 0.684** | | 0.344** | 0.163* | 0.079ns | -0.243** | -0.099ns |
| **PH** | 0.048** | 0.167** | 0.378** | 0.352** | 0.213** | 0.155** | 0.349** | | 0.225** | 0.106ns | 0.088ns | 0.013ns |
| **SPS** | -0.048** | 0.317** | 0.453** | 0.350** | 0.145* | 0.149** | 0.181** | 0.251** | | 0.437** | -0.054ns | -0.095ns |
| **SL** | -0.172ns | -0.031ns | 0.214ns | 0.347** | 0.226** | 0.114* | 0.113ns | 0.179** | 0.654* | | 0.024ns | -0.034ns |
| **FTPP** | -0.040ns | -0.071ns | -0.159ns | -0.193** | -0.221* | -0.145** | -0.301** | -0.109** | -0.040ns | 0.086ns | | 0.572** |
| **TNTPP** | 0.046* | -0.072** | -0.022ns | -0.087** | -0.105* | -0.140** | -0.102** | -0.016ns | -0.094ns | -0.075ns | 0.659** | |
| **Kps** | 0.062** | 0.265** | 0.536** | 0.719** | 0.630** | 0.577** | 0.556** | 0.257** | 0.527** | 0.378* | -0.065ns | -0.077** |

| | NDH | GFP | DM | ABM | GYPHa | HI | HLW | TKW | PH | SPS | SL | FTPP | TNTPP | Kps |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KPS | 0.236** | 0.058ns | 0.260** | 0.519** | 0.716** | 0.617** | 0.573** | 0.551** | 0.250** | 0.491** | 0.244** | -0.049ns | -0.076ns | |

**Note,** NDH= number of days to heading, GFP = grain filling period, DM= days to maturity, AGB= above ground biomass, GYPHa = grain yield per hectare, HI = harvest index, HLW = hectoliter weight, TKW= thousand kernel weight, PH= plant height, SPS = spikelets per spike, SL = spike length, FTPP= fertile tillers per plant, TNTPP = total number of tillers per plant.

**Genetic Divergence Analyses**
**4.5.1. Clustering of Genotypes**

Cluster analysis or clustering is the task of grouping a set of objects in such a way that objects in the same group (called a cluster) are more similar (in some sense) to each other than to those in other groups (clusters). Based on quantitative data, bread wheat genotypes were grouped by cluster analysis on the basis of Euclidean distances of similarity to their distinct groups. The $D^2$ values based on the means of genotypes resulted in categorizing the genotypes in to six clusters based on the result of principal component analysis (Eigenvalue ≥1). This is indication of the existence of genetic divergence among the tested bread wheat genotypes. Cluster analysis for 100 genotypes shows that Cluster I had 45 bread wheat genotypes (31.30%), Cluster II consisted of 33 (15.10%) and Cluster III had 15 (10.10%), Cluster IV consists of 2 (9.7%) and Cluster V consisted of 4 (6.9%) and cluster VI 1 (6.30%). It suggests that the crossing between genotypes of these clusters may yield better recombinant and superior high yielding segregants. Several authors previously reported presence of genetic divergence among bread wheat genotypes indicating need of clustering them in to distinct group. Ajmal *et al.,* (2013) classified 50 genotypes of wheat into 5 clusters. Salman *et al.,* (2014) classified 65 bread wheat genotypes into 6 clusters. Dargicho *et al.,* 2015b) also used 68 bread wheat germplasm and grouped in to six clusters. Devesh *et al.,* (2019) also classified 60 genotypes in to six clusters.

**Table 2: Cluster of tested genotypes at Holeta in 2021 main season**

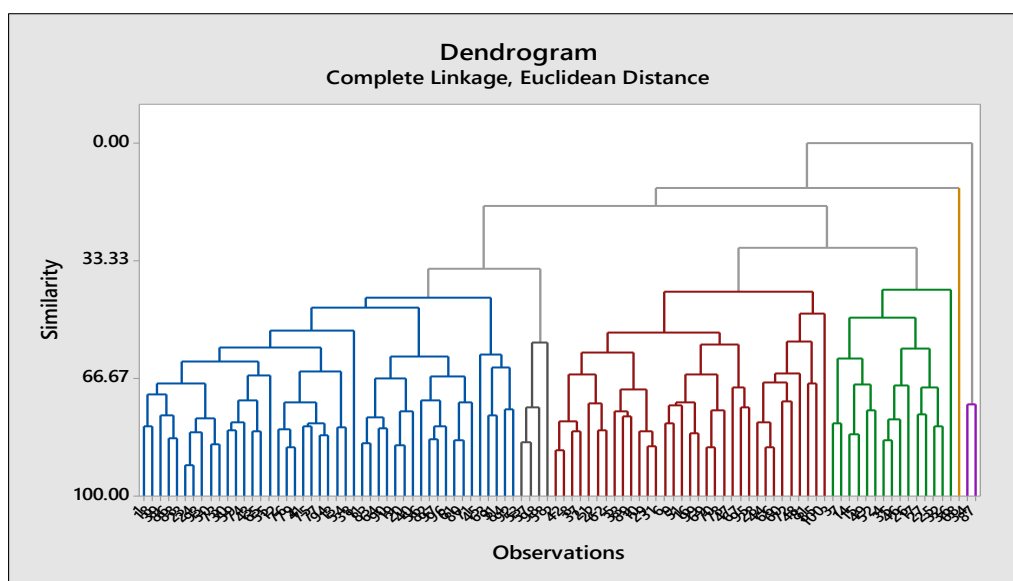| Cluster No. | No. of Genotypes | Proportion | Ave. distance from Centroid | Max. distance from centroid |
|---|---|---|---|---|
| Cluster1 | 45 | 40.75% | 3.01 | 5.2 |
| cluster2 | 33 | 25.95% | 2.95 | 5.01 |
| Cluster3 | 15 | 10.4% | 3.12 | 5.69 |
| Cluster4 | 2 | 9.70% | 1.69 | 1.69 |
| Cluster5 | 4 | 6.90% | 2.21 | 3.33 |
| Cluster6 | 1 | 6.30% | 0 | 0 |



**Figure 1: Dendrogram of cluster analysis based on fourteen quantitative traits**

# CONCLUSION

Wheat is one of the best useful crops grown in Ethiopia. Evaluation of correlation and Genetic Divergence analysis provides the basis for increasing yield and successful breeding programme. The study was carried out with the following objectives; to assess the association and Genetic Divergence analysis for yield and yield related traits like genotypic and phenotypic association and Genetic Divergence analysis of yield and yield related traits. The experiment was conducted by using ten by ten alpha lattice designs. Data were subjected to analysis of variance which revealed that there was highly significant difference) among the genotypes for all characters studied. The highest grain yield was recorded from Elit Ethiopia172/2020 and the lowest grain yield was recorded from 30HRWSN246/2019 genotype. Grain yield was positive and highly correlated with harvest index, thousand kernel weight kernels per, hectoliter weight, Plant height, spikelets per spike, and spike length, and negative and significant correlation with fertile tillers per plant. The highest cluster was cluster I which consists of forty five genotypes, and the lowest cluster was cluster VI consists of one genotype.

# REFERENCE

- Aremu, C. O. (2012). Exploring statistical tools in measuring genetic diversity for crop improvement. *Genetic diversity in plants*, 340-348.
- Awale, D., & Sentayehu, A. (2013). Genetic diversity in bread wheat (Triticum aestivumL.) Genotypes. *Pakistan Journal of Biological Science, 16*(21), 1330-133.
- Awale, D., Takele, D., & Mohammed, S. (2013). Genetic variability and traits association in bread wheat (*Triticum aestivum* L.) genotypes. *Int.Res. J. Agri. Sci, 1*(2), 19-29.
- Balcha, Y. (2002). Assessment of stability and character association in bread wheat (*Triticum aestivum* L.) genotype. M.Sc. Thesis. Alemaya University, Ethiopia.
- Chowdhry, M. A., Iqbal, S., Subhai, G. M., & Khaliq, I. (1997). Heritability for some quantitative characters in bread wheat. *J. Agri. Plant Sci, 7*(1-2), 27-28.
- Dargicho, D., Sentayehu, A., Firdisa, E., & Gezahegn, F. (2015). Genetic Variability in bread wheat (Triticum aestivum L.) germplasm for yield and yield Component traits. *Journal of Biology, Agriculture and Healthcare, 5*(17), 140-147.
- Desheva, G., & Cholakov, T. (2014). Variability, heritability and genetic progress for some Yield components in common winter wheat genotypes (*Triticum aestivum* L.) *Genetics and Plant Phys, 4*(3-4), 191-200.
- Foulkes, M. J., Slafer, G. A., Davies, W. J., Berry, P. M., Sylvester-Bradley, R., Martre, P., Calderini, D. F., Griffiths, S., & Reynolds, M. P. (2011). Raising yield potential of wheat. III. Optimizing partitioning to grain while maintaining lodging resistance. *J. Experi. Botany, 62*, 469-486.
- Karamanos, A. J., & Papatheohari, A. Y. (1998). Crop ecology production and management. *Crop Sci, 39*, 1792-1797.
- Khan, A. A., Alam, M. A., Alam, M. K., Alam, M. J., & Sarker, Z. I. (2013). Correlation and path analysis of durum wheat (*Triticum turgidum* L. var. *Durum*). *Bangladesh J. Agri. Res, 38*(3), 515-521.
- Mahalanobis, P. C. (1936). On the generalized distance in Statistics. *National Instit Sci India, 2*(1), 49-55.
- Majumder, D. A. N., Shamsuddin, A. K. M., Kabir, M. A., & Hassan, L. (2008). Genetic variability, response and path analysis of yield and yield contributing traits of spring wheat. *J. Bangladesh Agri. Univ, 6*(2), 227-234.
- Mollasadeghi, V., & Shahryari, R. (2011). Important morphological markers for improvement of yield in bread wheat. Advan. Envir. *Biology, 5*(3), 538-542.
- Morishima, H., & Oka, H. I. (1960). The pattern of interspecific variation in the genus *Oryza*: its quantitative representation by statistical methods. *Evolution, 14*(2), 153-165.
- Nei, M. (1973). Analysis of gene diversity in subdivided populations. *Proc Natl Acad Sci USA, 70*(12), 3321-3323.
- Obsa, C. H. (2014). Genetic variability among bread wheat (*Triticum aestivum*L.) genotypes for growth characters, yield and yield components in bore district, Oromia regional state. M.Sc. Thesis. Haramaya University, Ethiopia.
- Richard, R. A., Condon, A. G., & Rebetzke, G. J. (2001). Traits to improve wheat yield in dry environments. In: Reynolds M.P., Ortiz-Monasterio J.I. and McNab D.F. (eds.) Application of physiology in wheat breeding. CIMMYT, Mexico.
- Robertson, G. E. (1959). The sampling variance of the genetic correlation coefficient. *Biometrics, 15*, 469-485.
- Sadras, V. O., & Lawson, C. (2011). Genetic gain in yield and associated changes in phenotype, trait plasticity and competitive ability of South Australian wheat varieties released between 1958 and 2007. *Crop and Pasture Sci, 62*, 533-549.